RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
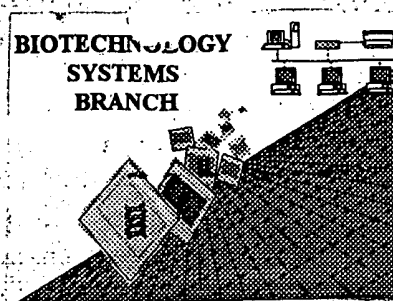BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/730,559_

Source: _OIPE_

Date Processed by STIC: _12/21/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/730,559_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

pp 1-24

Does Not Comply
Corrected Diskette Needed

```
            RAW SEQUENCE LISTING              DATE: 12/21/2000
            PATENT APPLICATION:  US/09/730,559   TIME: 09:06:46

            Input Set : A:\766.21 CIP sequence.txt
            Output Set: N:\CRF3\12212000\I730559.raw

     4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.,
     6 <120> TITLE OF INVENTION: IgA NEPHROPATHY-ASSOCIATED GENE
     8 <130> FILE REFERENCE: 11143
    10 <140> CURRENT APPLICATION NUMBER: US/09/730,559
    11 <141> CURRENT FILING DATE: 2000-12-07
    13 <160> NUMBER OF SEQ ID NOS: 121
    15 <170> SOFTWARE: PatentIn Ver. 2.0


ERRORED SEQUENCES

    17 <210> SEQ ID NO: 1
    18 <211> LENGTH: 4276
    19 <212> TYPE: DNA
    20 <213> ORGANISM: Homo sapiens
    22 <220> FEATURE:
    23 <221> NAME/KEY: CDS
    24 <222> LOCATION: (53)..(742)
    26 <400> SEQUENCE: 1
E--> 27 ttctaccgtt ttttccctgc tttctattcc aggtcagtct tcactgtttc cg atg gaa
    28 58
    29                                                          Met Glu
    30                                                            1
E--> 32 gat gga ttc ttg gat gat ggc cgt ggg gat cag cct ctt cat agt ggc
    33 106
    34 Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His Ser Gly
    35              5                  10                 15
E--> 37 ctg ggt tca cct cac tgc ttc agt cac cag aat ggg gag aga gtg gaa
    38 154
    39 Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg Val Glu
    40         20                  25                 30
E--> 42 cga tat tct cga aag gtg ttt gta ggc gga ttg cct cca gac att gat
    43 202
    44 Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp Ile Asp
    45     35                  40                 45                 50
E--> 47 gaa gat gag atc aca gct agt ttt cgt cgc ttt ggc cct ctg att gtg
    48 250
    49 Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu Ile Val
    50                 55                 60                 65
E--> 52 gat tgg cct cat aaa gct gag agc aaa tcc tat ttt cct cct aaa ggc
    53 293
    54 Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro Lys Gly
    55             70                 75                 80
E--> 57 tat gca ttc ctg ctg ttt caa gat gaa agc tct gtg cag gct ctc att
    58 346
    59 Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala Leu Ile
    60         85                 90                 95
```

58

106

global enor — see item 1 on Enor Summary Sheet

format enor

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
E--> 62 gat gca tgc att gaa gaa gat gga aaa ctc tac ctt tgt gta tca agt
     63 394
     64 Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val Ser Ser
     65     100             105             110
E--> 67 ccc act atc aag gat aag cca gtc cag att cgg cct tgg aat ctc agt
     68 442
     69 Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn Leu Ser
     70 115             120             125             130
E--> 72 gac agt gac ttt gtg atg gat ggt tca cag cca ctt gac cca cga aaa
     73 490
     74 Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro Arg Lys
     75             135             140             145
E--> 77 act ata ttt gtt ggt ggt gtt cct cga cca tta cga gct gtg gag ctt
     78 538
     79 Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val Glu Leu
     80             150             155             160
E--> 82 gcg atg gta atg gat cgg cta tac gga ggt gtg tgc tac gct ggg att
     83 586
     84 Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala Gly Ile
     85             165             170             175
E--> 87 gat acc gac cct gag cta aaa tac cca aaa gga gct ggg aga gtt gcg
     88 634
     89 Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg Val Ala
     90     180             185             190
E--> 92 ttc tct aat caa cag agt tac ata gct gct atc agt gcc cgc ttt gtt
     93 682
     94 Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val
     95 195             200             205             210
E--> 97 cag ctg cag cat gga gag ata gat aaa cgg gta agc ctt ata cta cat
     98 730
     99 Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile Leu His
     100             215             220             225
E--> 102 ttt gga aaa ttc tagaaatggt cctctaaatg tgtgattacc aatattagaa
     103 782
     104 Phe Gly Lys Phe
     105             230
E--> 107 cgggagcatt ttatgacaat aaagtgacag ctgacaattt tgcctataga gttaattatg
     108 842
E--> 110 gtctataata catgaaataa tgtcctatga atttctttta tctttcagtt ttttgagtag
     111 902
E--> 113 cctaatcaga acactacaat ttacttgagt taatttaatc ttctctaact tccattcaat
     114 962
E--> 116 ctcaatccat ccgtccattc attcacttag tttgtaagtc attcaataaa tatttactga
     117 1022
E--> 119 atcctttgtt ctgtgttata tcaagtatac aaacaggaat gcccttgagg tttcctgccc
     120 1082
E--> 122 tttttttgt ttgttttta atcctgggac atagggaaga cctcagcaag ccctatttct
     123 1142
E--> 125 caatgaattg tactcacaga tttctttttt tttttttttt tctttttcca cagccgccac
```

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
      126 1202
E--> 128 ctctcaccga tttattcctt agcttggtgt ttcatgtatt caacaaacgt tttagtgctt
      129 1262
E--> 131 agggcaagaa gttcctgtcc tcatgagttt atttcctagc agatagaact gtatcacttg
      132 1322
E--> 134 ccagtactac tcagagtgtg gcctgtggac tgacctccag tctgtaaact tagtttgtag
      135 1382
E--> 137 tgagatagga atttagacca gaatgtgtaa tcaaccacat tactgggcac aatgtttggt
      138 1442
E--> 140 ccagctggcg attttttttt catagaaagc ctttattgat gagggaagca atatattgat
      141 1502
E--> 143 ttatattttg gggtcacctt tttatttcat ggcacactgg cactttcatg catgctgact
      144 1562
E--> 146 ttgatatcca tcactctgag gcattgtgct aaaatagatt gattttatcg tgttgttctc
      147 1622
E--> 149 aattcaagat gtaaaaatca tcaagtcagt agcagttttt gctttttatg tttcatgtca
      150 1682
E--> 152 tgtacagtct acttcactgg cagtaaaaaa atttaagata gtggtggtca tcctacaaac
      153 1742
E--> 155 tgtgaatcta ttaaagagaa aagtatctgt tctattctaa gcatggggga gggacaagat
      156 1802
E--> 158 tagtatgtta acatgcctac tttgtttgtt tgagatggag tctctctccg tcacccaggc
      159 1862
E--> 161 tggagtgcag tggtacagtc tcagctcact ccaacctctg cctcccgggt tcaagtgatt
      162 1922
E--> 164 ctcctgcctt agcctcccga gtaggtggaa ttacaggcat ataccaccat gcccaacaaa
      165 1982
E--> 167 tgtttgtatt tttagtggag acagggtttc accgtgttgg tcaggccagt ttcaaactcc
      168 2042
E--> 170 tgacctcaag ggatccacct gcctcacccc ctcaaagtgc tgggattaca ggcatgagcc
      171 2102
E--> 173 acccaccatg cctggcctac ttggtttttt atgcacacta aaaaatacct acatctcact
      174 2162
E--> 176 gccttattcc aacataagtt tcagagctgt gggattggtc attagaaatt cagactgaat
      177 2222
E--> 179 ttgtgttcct ctgcaatgaa atcctttgcc cagtgttcat gtcactctgt agacattatg
      180 2282
E--> 182 gagcagccta gaggccagaa gcccagtgct ctccttatgc ctgctcttcc tgggcttcgt
      183 2342
E--> 185 gacactcttc ttctcctttt gtacttttat ttttttagtt aaaaaatttt ttttagaggg
      186 2402
E--> 188 agggtctcac tctgtcaccc aggctggagc acagaatcac aatcatgact cactgcatgt
      189 2462
E--> 191 tcttctcctt ttgttcatgg ctaatcttgg tcaggattcc ttgtcagagc tgggtggcac
      192 2522
E--> 194 cagtgctggt gacagcctgc tgtaagggag tttcagccat gaatctctcc agactaaaaa
      195 2582
E--> 197 taaccagctc tttttctagct gatgaattaa taaccaggtg actgttaatg cttgaaaggt
      198 2642
```

```
E--> 200 tcacatgaca ggttggccga tagaacgctg gaacaggccc agttttagaa attcacctct
     201 2702
E--> 203 gacttttaga ctcaggtgaa ccattcttac tgagaaagaa caaagcaggg ttttagactg
     204 2762
E--> 206 tgaatcctat ggctgcatct tttttttttt tttaacgag ttccaggttt gtgattataa
     207 2822
E--> 209 cccaacatgt gtacactata aatagaaacc acgagccagg cttttttacga cagctcagaa
     210 2882
E--> 212 tcttgtgacg cagtagtcag gcatcttcac accgacttga atattgaagt gcagttgtgt
     213 2942
E--> 215 ggaacttgga tcatcttagt tgattttgtt taaattatga ttccacatat gacaaaaatc
     216 3002
E--> 218 cagatccact aattaaaatg agggtttatg tctatgaata atctcctgtg ggtttaatct
     219 3062
E--> 221 cataacattc tagtctaaac agttggcttc acttcatgat gtctgctcaa atcctttttc
     222 3122
E--> 224 ctttaaagga tgtttatttta ataagaaaaa aaatgtaaaa tgatagataa taaaagcctt
     225 3182
E--> 227 actaggttct taaaagatga actatccata tttcagtaaa tgaataatta gtccttcctc
     228 3242
E--> 230 tttgggcacc ttggaacaga ttcattcaga tagtgggtgg aaatgtacat gtatggtaag
     231 3302
E--> 233 cattgctggc ctagtcactg aaaaatgtaa actcttattt·ttgattgcag gtggaagtta
     234 3362
E--> 236 agccatatgt cttggatgat cagctgtgtg atgaatgtca gggggcccgt tgtggggga
     237 3422
E--> 239 aatttgctcc atttttctgt gctaatgtta cctgtctgca gtattactgt gaatattgct
     240 3482
E--> 242 gggctgctat ccattctcgt gctggcaggg aattccacaa gcccctggtg aaggaaggcg
     243 3542
E--> 245 gtgaccgccc tcggcatatt tcattccgct ggaactaaag gataactgca gtgctcattt
     246 3602
E--> 248 tcaggcctca gaataagtgc actcttctgt tcattctgac cccttcctca acctcttcac
     249 3662
E--> 251 gctggcatgt cctttgtag cagtctgtaa cttaactata gtataatgaa aagaatgacc
     252 3722
E--> 254 tataatatag gtgttttgta gattcttgtg tcactgcaaa caatatgaac tccttttcg
     255 3782
E--> 257 tattgccatc gggttgcatg gaagtttat tctcttgttt tgctggaaac caagaggatc
     258 3842
E--> 260 caaacttcct gcaacatttt cttagaggag agagagaaat attaaaagag aaatgaaaca
     261 3902
E--> 263 atagagtatt ttgggttttt aattaaatta ttgttaataa tataacatat aagaatactt
     264 3962
E--> 266 ttattaaaat aaccatgcaa caataacact atcggtctat ctgacagttt ttcccccagg
     267 4022
E--> 269 gaagtgcttt tgcctttcc tttctttttt tttttttttc atctttttg ttctctctct
     270 4082
E--> 272 tttttccatc ccttttttaat tttttaaca gcaatggagg aagttaacaa tttttaatgg
```

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
       273 4142
E--> 275 aaagagcatg ttagagcaaa caaatgcata agcaagactg agcagcatta taattaattt
       276 4202
E--> 278 tcaggtgttt gaggctgaac ataatttcat tatccctcaa aaagttacca ccacatcaga
       279 4262
E--> 281 aaaaaaaaaa aaaa
       282 4276
       285 <210> SEQ ID NO: 2
       286 <211> LENGTH: 2689
       287 <212> TYPE: DNA
       288 <213> ORGANISM: Homo sapiens
       290 <220> FEATURE:
       291 <221> NAME/KEY: CDS
       292 <222> LOCATION: (107)..(535)
       294 <400> SEQUENCE: 2
E--> 295 gttggaggtt ctggggcgca gaaccgctac tgctgcttcg gtctctcctt gggaaaaaat
       296 60
E--> 298 aaaatttgaa ccttttggag ctgtgtgcta aatcttcagt gggaca atg ggt tca
       299 115
       300                                                       Met Gly Ser
       301                                                         1
E--> 303 gac aaa aga gtg agt aga aca gag cgt agt gga aga tac ggt tcc atc
       304 163
       305 Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile
       306         5                    10                   15
E--> 308 ata gac agg gat gac cgt gat gag cgt gaa tcc cga agc agg cgg agg
       309 211
       310 Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser Arg Arg Arg
       311 20                   25                   30                   35
E--> 313 gac tca gat tac aaa aga tct agt gat gat cgg agg ggt gat aga tat
       314 259
       315 Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr
       316                   40                   45                   50
E--> 318 gat gac tac cga gac tat gac agt cca gag aga gag cgt gaa aga agg
       319 307
       320 Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg
       321               55                   60                   65
E--> 323 aac agt gac cga tcc gaa gat ggc tac cat tca gat ggt gac tat ggt
       324 355
       325 Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly
       326               70                   75                   80
E--> 328 gag cac gac tat agg cat gac atc agt gac gag agg gag agc aag acc
       329 403
       330 Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr
       331         85                   90                   95
E--> 333 atc atg ctg cgc ggc ctt ccc atc acc atc aca gag agc gat att cga
       334 451
       335 Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg
       336 100                 105                 110                 115
```

```
E--> 338 gaa atg atg gag tcc ttc gaa ggc cct cag cct gcg gat gtg agg ctg
     339 499
     340 Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp Val Arg Leu
     341           120             125             130
E--> 343 atg aag agg aaa aca ggt gag agc ttg ctt agt tcc tgatattatt
     344 545
     345 Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser
     346           135             140
E--> 348 gttctcttcc ccattcccac ctcagtccct aaagaacatc ctgattcccc cagtcttcaa
     349 605
E--> 351 gcacatgaat tcagaatgaa aggtttgcca tggctaagga atgtgactct ttgaaaacca
     352 665
E--> 354 tgttagcatc tgaggaactt ttttaaactt tgttttaggg acttttttttt ccttaggtaa
     355 725
E--> 357 gtaatgattt ataaactcct ttttttttttt ttgactatag tcggttgcat ggttacttta
     358 785
E--> 360 agcgtggaat caaatggagt ggcatttagt tcaggcggct tgttccttgc catggcaaag
     361 845
E--> 363 tatcaagaag atccccaagt caagtcacat ttgtaaagct gcttcccaat tggctttgtc
     364 905
E--> 366 acgcagtgtt gaagcagtgg gagagagatt cacctgttat aaaggaactg actaacacaa
     367 965
E--> 369 gtatcccgtc tatatctgaa tgctgtctct aggtgtaagc cgtggtttcg ccttcgtgga
     370 1025
E--> 372 gttttatcac ttgcaagatg ctaccagctg gatggaagcc aatcaggttg cttcactcac
     373 1085
E--> 375 caagtctaga tattcatgaa aatggaacaa gtctgtacaa ttttaaaaaa aggttgaagg
     376 1145
E--> 378 agtggtttgt tccaaggag tgactttttt ttaaaaaaaa aagctttgta tatattaaaa
     379 1205
E--> 381 ttgatgttac tagaataagt acagtaccaa ggacttcatt atagaatttg ttctgccttt
     382 1265
E--> 384 aaacatggct acctacctgg cagggctttg ttaactactg aatacctgtc tggtaatcac
     385 1325
E--> 387 taaaacatct taatgtttcc ctttttttcta gtttgttata ttcctattat gtccattgag
     388 1385
E--> 390 agtaagctta gtatatcaaa ctctccattt gacagtgaag agaacatagt gaaagtctgt
     391 1445
E--> 393 ggcggcattt ttataagtaa ttccttattt ctgcctgaag accacaaagc ctcctggagg
     394 1505
E--> 396 cgtaactgct cagaccggtc ttcagggaat atttaaggac ttagtggaat ttatgaacaa
     397 1565
E--> 399 taagtctgat gagattagcc tgggagtggt gtcctgcagc tgtctaatct agttagagtg
     400 1625
E--> 402 gcattaacat tctaatctcc ttgagaatgc cttttatagt ctgttcaaag caagtcattg
     403 1685
E--> 405 atggttcttc gaggtagtgt taactgaagt gttcttcagt ttgtcaagat aatgttcagt
     406 1745
E--> 408 gcttggcact aaataacat tttttgcaag aactccaagg cacattattg aatgcctta
```

```
      409 1805
E--> 411 accaagtgca ttctgggaag tttgcttgac tcattatctt gcttttctgc agcattctgt
      412 1865
E--> 414 gatttgagtc atccatgaat ccatgaataa aagttacatt ctttgattgg taatattgcc
      415 1925
E--> 417 atttataaca agactcacta atgagggtat cactttgact gactgatttg ttaaagtttt
      418 1985
E--> 420 taagcctctc attttcctaa cccagaaatc acagcctgat tttattaaaa gtagagcttc
      421 2045
E--> 423 attcatttca taccatagat accatcctag taaatccaga acatatacaa ggttcatgtg
      421 2105
E--> 426 agtctgcttt cttgacatga tagcattgtt tgatgcagtg gatatgtcag aatgactaac
      427 2165
E--> 429 ctaggagttt aaaactccta agaaactaaa acctgtaaga catttaaaag tctccacaat
      430 2225
E--> 432 tttaatgtat acaaagctat gttactgtgt aacacattac agttcaaatt cactccagaa
      433 2285
E--> 435 ataaaaggcc agtaggatta gggactcact ggtagtttgg agtctcccag cacacatccc
      436 2345
E--> 438 tcctagtggg atgatctatt cacatatctc ccagcttttt tattttttgct tctgtatatc
      439 2405
E--> 441 acagtgagtg gatggccctt cagctttttc tctcctggcc agacatgcag tcttgccttt
      442 2465
E--> 444 agatatcgca gagacaaaat tcacagcatg tcttaaatct tccaggattt gcaagaacca
      445 2525
E--> 447 aattgctcaa cagtatgtat gtttagaggg gttagactcc tttttaaaat ctggatatct
      448 2585
E--> 450 aaccacctac ttaaatctgt ttgatagtgt caaaccaccc ccacccttga tcctcccacc
      451 2645
E--> 453 cccaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
      454 2689
      457 <210> SEQ ID NO: 3
      458 <211> LENGTH: 2981
      459 <212> TYPE: DNA
      460 <213> ORGANISM: Homo sapiens
      462 <220> FEATURE:
      463 <221> NAME/KEY: CDS
      464 <222> LOCATION: (1297)..(1608)
      466 <400> SEQUENCE: 3
E--> 467 cctctctctc tctttcacag agtcttgctc tgtcgcccag gctggagtgc agtggcacaa
      468 60
E--> 470 tctcactgca agctccgcct cctgggttca cgccattctc ctgcctcagc ctcccaaata
      471 120
E--> 473 gctgggacaa caggcacctg ccaccacgcc cggctaattt tttgtatttt tagtagagac
      474 180
E--> 476 agggtttcac catgttagcc aggatggtct caatctcctg acctcgtgat ccacccgcct
      477 240
E--> 479 cagcctccca aagtgctgag attacaggtg tgagccacca cgcccagcca catctttctt
      480 300
```

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
E--> 482  tctttctttt tggttttttgt ttgttgtttg agacagggtc ttgctctgtc gccctggctc
     483  360
E--> 485  acgtgaacct cccacctcag cctcccaagt agctgagacc acaggtgtga gccaccactc
     486  420
E--> 488  ctgggtaatg tttgtatttt tttgtagaga tggggtttca ccgtgctgcc cagactgctc
     489  480
E--> 491  tcaaactcct gggctcaagt gatccacctg ccttgacctc ctaaagtgct ggaattacag
     492  540
E--> 494  gtgtgagcca ccgtgctcag ccgagtgtct ttcgtatgtt ttctgagcac gtggatttcc
     495  600
E--> 497  atctctctgc attctctgtt catctcagcc tgtttgttcc attgagataa atgacttttt
     498  660
E--> 500  cttggtaact tagagtactt tgtgtattta caggttaatc ccttatcaat ttatatcagt
     501  720
E--> 503  tgctgctatc ttttcttaga ttttctttt cattttaaaa attacattgt ttcaatgaac
     504  780
E--> 506  agaatttta agtttaacg tagtccactt tgtccatttt ctttatgacc ggtgcatttt
     507  840
E--> 509  agggtcttgt ttaagaaatc gttctttatc ctgaggtcat aaagatagtc tactgtattt
     510  900
E--> 512  tcttttaaga gctgaaaagg tgttttatat ttaatttatt tgggattggc ttttgtgtgg
     513  960
E--> 515  tggggataag gatcacaatt ttatttcatt ttttttccac ttggttatgc cagtggcccc
     516  1020
E--> 518  atttccattt tttgaatagt ctttctgtgc agaaaagact tcactagcag agaagtcctg
     519  1080
E--> 521  agacttaccc ttcaaaaggc cccattcaca aggctagcac ttggcgtgca tctgagaacc
     522  1140
E--> 524  tggattttgg ggtggttcct ataatgtggt gtatgctgaa cacccacctt tccttctggg
     525  1200
E--> 527  agtctggaat ttgggtatat gttggacaga ggctgcctaa gtgaccagct tcaacaacag
     528  1260
E--> 530  ccctgggtgc tgggtcactc atgacccata gacaaa atg cca cac atg ttg tca
     531  1314
     532                                        Met Pro His Met Leu Ser
     533                                         1               5
E--> 535  cag ctt att gct gga gga gtt agc aca tcc tgt gtg act gca ctg gga
     536  1362
     537  Gln Leu Ile Ala Gly Gly Val Ser Thr Ser Cys Val Thr Ala Leu Gly
     538             10              15              20
E--> 540  gag gaa act ggt gcc tgg ttc cct gtg tat ttg tcc cac gcc tcc agt
     541  1410
     542  Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr Leu Ser His Ala Ser Ser
     543             25              30              35
E--> 545  ccc ttt gct gat ctc gtt ttt tgt cct ttt gct gag ata aat cac agc
     546  1158
     547  Pro Phe Ala Asp Leu Val Phe Cys Pro Phe Ala Glu Ile Asn His Ser
     548             40              45              50
E--> 550  cag gag tat gac aat atg cgg ggt cct gtg agt cct cct aac aaa cag
```

```
                 RAW SEQUENCE LISTING              DATE: 12/21/2000
                 PATENT APPLICATION:  US/09/730,559  TIME: 09:06:46

                 Input Set : A:\766.21 CIP sequence.txt
                 Output Set: N:\CRF3\12212000\I730559.raw

         551 1506
         552 Gln Glu Tyr Asp Asn Met Arg Gly Pro Val Ser Pro Pro Asn Lys Gln
         553  55                  60                  65                  70
E--> 555 ttc aat ctg ggg gtg atc ttt ggg atc ccc aac aac tgt cgt ttc ccc
         556 1554
         557 Phe Asn Leu Gly Val Ile Phe Gly Ile Pro Asn Asn Cys Arg Phe Pro
         558                  75                  80                  85
E--> 560 act gat aat aaa ata act gag aag cag cta ttg ggc aat gtt ctg aac
         561 1602
         562 Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu Leu Gly Asn Val Leu Asn
         563                  90                  95                  100
E--> 565 tac cct tgaacattca tgtcttcatc tgaacatcca tctactaccc ctgatttttt
         566 1658
         567 Tyr Pro
E--> 569 cagtgcaggg tgcatatcct gtatcaccca ataaatggtc attgatcacc ataggaaagg
         570 1718
E--> 572 aacagtgaaa gctccacggt ggtttggagg aaggtggcag gcattcagcg gtaacttttt
         573 1778
E--> 575 tgagcagata gattttatgt ttttgcaatg agtgaaataa attttcccat atctatttaa
         576 1838
E--> 578 ggttggcaat cattatcttt ttatcatctt ggaacatttg gaattccttt aatatgttta
         579 1898
E--> 581 gttaggaatt ttctaccttc ctcatcttgt ccgatagttt aaaatcccac agttatttca
         582 1958
E--> 584 cgggctcctc atacctgcct gtgtgatttc taacatgtca cgctatgcaa ccagttgctt
         585 2018
E--> 587 ttacttgtag agtgtttctt taggtaatag cttattattg gttatgtgat tacagtgtgt
         588 2078
E--> 590 taaagacagg tctgtagtta tgtaaaatgc cgtttctctg agtatcatgg tcatttccac
         591 2138
E--> 593 atatttctct attcatgtat ttgtaagaat atatctattt ttgcagtatt ttatttattt
         594 2198
E--> 596 attttatttt attttctgaa acggagcctt gttctgtcac ctaggctgga gtgcagtggt
         597 2258
E--> 599 gtgatctcga ctcactgtga cctccccctc ccaggttcaa gcgattctcc cgcctcatcc
         600 2318
E--> 602 tcccaagtca ttgggattac agtcacgtgc catgaagccc tgctaatttt ttgtattttt
         603 2378
E--> 605 agtagagaca ggatttcacc atgttggcga tgctggtttc gaactcctgg tttcgaactc
         606 2438
E--> 608 ctgacctcaa gtgatccacc tgcctcggcc tcccaaagaa ctgggattat gggcgtgaac
         609 2498
E--> 611 caccacgcca ggtcagtttt gcagtgtttt aaatactgtt gtctttgaga ggagagaggc
         612 2558
E--> 614 acgcacatag actatggtga ttaccatcat atactggaaa gtgcaaagtg tagcgcagtt
         615 2618
E--> 617 aactgtgagc catctcatca aaccctaaca gatgtctcat ttgtccataa aggggcttct
         618 2678
E--> 620 gtcccataga aattcatgta cccaacctac tcttcaacca tgattttct ctgatggcct
```

```
        621 2738
E--> 623 gtgtgaacag attaatggtg tccatctaat tccttcccca ctgggggaaa gcaaatcatc
        624 2798
E--> 626 aggcccattg caaaaactgc tcttggttga gcttcctgcc ttaaatcata cccacagtga
        627 2858
E--> 629 atggcgtccc tttatcaccg ctaatgactc tgacatctct ctccactcac atgtgagcct
        630 2918
E--> 632 cctcagctct cgataaacaa gtctgtctcg gttcatttat tctacaaaaa aaaaaaaaaa
        633 2978
E--> 635 aaa
        636 2981
        639 <210> SEQ ID NO: 4
        640 <211> LENGTH: 1461
        641 <212> TYPE: DNA
        642 <213> ORGANISM: Homo sapiens
        644 <220> FEATURE:
        645 <221> NAME/KEY: CDS
        646 <222> LOCATION: (282)..(680)
        648 <400> SEQUENCE: 4
E--> 649 aattcggcac gagcagcttt ctagttggat taggcaacag aatcctttga aaatgtgtgt
        650 60
E--> 652 gcacagacca ggtggctctc tgggccagtg tactctgaaa gatgtgtgtc ctggcctagc
        653 120
E--> 655 tggttgagga aaagcagggc aagcctagcc aaatcacaca tcttgaacag ccctcattcg
        656 180
E--> 658 ttatactaac tttcccacct tctggtgtgt ataggagata aagatggcag acgtgctatt
        659 240
E--> 661 aggctgccaa tgggagtggg ctctgatatg gtctttcaaa t atg aat cac ccc tgg
        662 296
        663                                             Met Asn His Pro Trp
        664                                             1               5
E--> 666 cat gtg tgt ttc ctg ttt aag gtt ctc agg tat tac cca act gca cca
        667 344
        668 His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro
        669                10              15                  20
E--> 671 ata tta aaa tgg aca cat acc gtg tca tgc agt tgg tgc cga agt gtt
        672 392
        673 Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val
        674                25              30                  35
E--> 676 tta agg gaa gtt gta ggc aat gtg agt tta tca gaa aac ttc acc ata
        677 440
        678 Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile
        679                40              45                  50
E--> 681 tca gca ttt tgc cct gag ctt aca cca ttc cca gat caa ggt aca agc
        682 488
        683 Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser
        684    55              60                  65
E--> 686 aca atg att tcc ttt ctt gaa aag ttc aac aaa agc aag aga gag aga
        687 536
```

```
    688 Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg
    689 70                75                80              85
E--> 691 ttg gag ttg atg ctg cat ttt tat tct gtg tta agt ctt gaa cct gct
    692 584
    693 Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala
    694                90                95              100
E--> 696 gtt gct gaa cat tgg tca ggg gaa ttt gag aag tgg aaa gtg ggc ttt
    697 632
    698 Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe
    699                105               110             115
E--> 701 ttt cac cct ttg aaa aga gag gat gga ttc ttc acc aga act gac att
    702 680
    703 Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile
    704                120               125             130
E--> 706 taaaaaaagt cagcgtggca cgttttagta tgtgtggcag atctaaasag acaatatttt
    707 740
E--> 709 gatctcagga gtgtttattc ttgaaccatt ttcagaactc taagatttga gaaataataa
    710 800
E--> 712 aatattgacc atccttcaaa gagaaaaaca cagggcgatc tttggcatag cctgtcattt
    713 860
E--> 715 tgctcacatt tcacttctct ctctccaact tcagagcccc tgctgtggaa caggtgctgt
    716 920
E--> 718 gctgggtggc aggggaggtc tctggctttt ttttttttttg atctccgtct taacatctag
    719 980
E--> 721 cctactggag gaagtgtatt taatcatcca cttatctgtt aacaattatc tctgagggcc
    722 1040
E--> 724 cgtcacattc agagaagatt ctaggttctc tacaagtatc ctctcactgt gtacatacta
    725 1100
E--> 727 aatcaacatc ctgctggatt tcccccagac atctccttc atcaccattg gagagtatcc
    728 1160
E--> 730 tctaattgcc agccctattc accatactca tctcatttga tctggagttt tctgagagtg
    731 1220
E--> 733 accgggggtg ggatggacag gataatttag caagagtgta taagtaaaat ctatataata
    734 1280
E--> 736 aaagttatct ccctgtgccc cccatgatct attctttatg tagcagtctg aatgagattt
    737 1340
E--> 739 tcagaaacaa gaaccacttt accttagtct cttcttcttc ttcttcttct tttcttttct
    740 1400
E--> 742 ttttttttag tattatgggc aacagagcaa gacccagtct caggaaaaaa aaaaaaaaaa
    743 1460
E--> 745 a
    746 1461
    749 <210> SEQ ID NO: 5
    750 <211> LENGTH: 3329
    751 <212> TYPE: DNA
    752 <213> ORGANISM: Homo sapiens
    754 <220> FEATURE:
    755 <221> NAME/KEY: CDS
    756 <222> LOCATION: (637)..(1035)
```

```
                    RAW SEQUENCE LISTING              DATE: 12/21/2000
                    PATENT APPLICATION:  US/09/730,559   TIME: 09:06:46

                    Input Set : A:\766.21 CIP sequence.txt
                    Output Set: N:\CRF3\12212000\I730559.raw


        758 <400> SEQUENCE: 5
E--> 759 ccaaagtgct gggattatag gcatgagcca ctgcgcccgg ccagaatacc ctatccttaa
    760 60
E--> 762 acatgaattt aggggagggg aggacacaat tcaatctata acaactatca ctggctgatt
    763 120
E--> 765 ttggcagagg cctgtggcct ccagtatttt gagggagctg agggccactg atctctccat
    766 180
E--> 768 atgctctcaa catcatggga ctagtaggat gaaagcaagc ctcagaccag attctacctc
    769 240
E--> 771 aagcaggcac acaaacattc atgcagcttc tacttggagc ctgatgaagt tcaaattgtt
    772 300
E--> 774 tgtcctctga ggctctcttt gcatggaaat ttctcccatg acagatgaga aagttctggg
    775 360
E--> 777 gcagcattca gctttctagt tggattaggc aacagaatcc tttgaaaatg tctgtgcaca
    778 420
E--> 780 gaccaggtgg ctctctgggc cagtgtactc tgaaagatgt gtgtcctggc ctagctggtt
    781 480
E--> 783 gaggaaaagc agggcaagcc tagccaaatc acacatcttg aacagccctc attcgttata
    784 540
E--> 786 ctaactttcc caccctctgg tgtgtatagg agataaagat ggcagacgtg ctattaggct
    787 600
E--> 789 gccaatggga gtgggctctg atatggtctt tcaaat atg aat cac ccc tgg cat
    790 654
    791                                             Met Asn His Pro Trp His
    792                                               1                 5
E--> 794 gtg tgt ttc ctg ttt aag gtt ctc agg tat tac cca act gca cca ata
    795 702
    796 Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro Ile
    797              10                  15                  20
E--> 799 tta aaa tgg aca cat acc gtg tca tgc agt tgg tgc cga agt gtt tta
    800 750
    801 Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val Leu
    802         25                  30                  35
E--> 804 agg gaa gtt gta ggc aat gtg agt tta tca gaa aac ttc acc ata tca
    805 798
    806 Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile Ser
    807     40                  45                  50
E--> 809 gca ttt tgc cct gag ctt aca cca ttc cca gat caa ggt aca agc aca
    810 846
    811 Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser Thr
    812 55                  60                  65                  70
E--> 814 atg att tcc ttt ctt gaa aag ttc aac aaa agc aag aga gag aga ttg
    815 894
    816 Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg Leu
    817             75                  80                  85
E--> 819 gag ttg atg ctg cat ttt tat tct gtg tta agt ctt gaa cct gct ttt
    820 942
    821 Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala Phe
    822             90                  95                 100
```

```
                 RAW SEQUENCE LISTING              DATE: 12/21/2000
                 PATENT APPLICATION:  US/09/730,559    TIME: 09:06:46

                 Input Set : A:\766.21 CIP sequence.txt
                 Output Set: N:\CRF3\12212000\I730559.raw

E--> 824 gct gaa cat tgg tca ggg gaa ttt gag aag tgg aaa gtg ggc ttt ttt
     825 990
     826 Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe Phe
     827          105                110                115
E--> 829 cac cct ttg aaa aga gag gat gga ttc ttc acc aga act gac att
     830 1035
     831 His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile
     832          120                125                130
E--> 834 taaaaaaagt cagcgtggca cgttttagta tgtgtggcag atctaaagag acaatatttt
     835 1095
E--> 837 gatctcagga gtgtttattc ttgaaccatt ttcagaactc taagatttga gaaataataa
     838 1155
E--> 840 aatattgacc atccttcaaa gagaaaaaca cagggcgatc tttggcatag cctgtcattt
     841 1215
E--> 843 tgctcacatt tcacttctct ctctccaact tcagagcccc tgctgtggaa caggtgctgt
     844 1275
E--> 846 gctgggtggc aggggaggtc tctggctttt ttttttttgat ctccgtctta acatctagcc
     847 1335
E--> 849 tactggagga agtgtattta atcatccact tatctgttaa caattatctc tgagggcccg
     850 1395
E--> 852 tcacattcag agaagattct aggttctcta caagtatcct ctcactgtgt acatactaaa
     853 1455
E--> 855 tcaacatcct gctggatttc ccccagacat ctcccttcat caccattgga gagtatcctc
     856 1515
E--> 858 taattgccag ccctattcac catactcatc tcatttgatc tggagttttc tgagagtgac
     859 1575
E--> 861 cgggggtggg atggacagga taatttagca agagtgtata agtaaaatct atataataaa
     862 1635
E--> 864 agttatctcc ctgtgcccce catgatctat tctttatgta gcagtctgaa tgagattttc
     865 1695
E--> 867 agaaacaaga accactttac cttagtctct tcttcttctt cttcttcttt tcttttcttt
     868 1755
E--> 870 ttttttagta ttatggggat ctgtttctgt tgcccaggt ggagtgcagt ggtatgatct
     871 1815
E--> 873 tggctcacag cagccttgaa ctcccgggct caagtggtcc tcctgcctct gcttccctag
     874 1875
E--> 876 tagctaggac tgcaggtttg tgccaccaca cctggctaat tgaaaaaaga aatttttttt
     877 1935
E--> 879 caatagagac agtgtcttgc tatgtcccca ggctggtctc aaactcctgg cctcaagtga
     880 1995
E--> 882 tcctcctgtc tcatcctccc aaagtgttgg aattacaggt gtgagctact atactcggcc
     883 2055
E--> 885 agtacccttc tcaaaacact tcagcacttc ccattgcact tgggttgaaa ttcccaccac
     886 2115
E--> 888 tcactggggc ccacaagact cttcaagact gaatccttgc tcaacattgt gacctgcccc
     889 2175
E--> 891 ctaccacctg cagcctcact tgctgtgctc cagccatgtg gatcttcctc ctgtctctaa
     892 2235
E--> 894 aactgcctca ggtcatttgc acctgctgtt cttcccaaag gctgtgtgat ttccatcagt
```

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
        895 2295
E--> 897 cagtcttagc tcgtatacct ccttggagac acctcttctg accaaccagt ccaaagaatc
        898 2355
E--> 900 tcctcttatc atgtcactct gttttattta tttatttaga gatggagtct cgctctgtca
        901 2415
E--> 903 cccaggctgg agtgcagtgg cgcgatctct gctcactgca agctccacct cctgggttca
        904 2475
E--> 906 tgccgttctc ctgcctcagc ctcctgagta actgggacta tgggcaccca ccactacacc
        907 2535
E--> 909 cggctaattt tttgtatttt tagtggggat ggggtttcac tgtgttagcc aggatggtct
        910 2595
E--> 912 tgatctcctg accttgtgat ctgcctgcct ccacctccca aagtgtttta tttattttaa
        913 2655
E--> 915 aggcatgtat cactctctga aaattagctt ctttcttctt tttccttgtt atcatccatt
        916 2715
E--> 918 tccccgaacc agaatagaag ttcctgaggc cagaacttct gtctctctgc ccctcactat
        919 2775
E--> 921 gtgtctctgg cacataccccc agtgcctgcc tgctctaaag taaaatctta gtaaatatta
        922 2835
E--> 924 ctgttgacta aataaatgaa taaatccctt ttaatgcccc tttggaagtt gccaagtaaa
        925 2895
E--> 927 gaataggatc ccttttttaag attacacttt tggctattga tctgtgtgtc tggaacaaga
        928 2955
E--> 930 tacagtttga agatactacc atgggacatg acatcagttg agctgattaa ggttttagta
        931 3015
E--> 933 ataagaatcc aggatgtgtc cgggtgcggt gctcacgcct gtaatcctag cattttggga
        934 3075
E--> 936 gaccgaggcg ggcagatcac gaggtcagca gtttgagacc agcctgacca acatggtgaa
        937 3135
E--> 939 accccgtctc tactaaaaaa tacagaaatt agccgggtgt ggtggtgtcc acctgtagtc
        940 3195
E--> 942 ctagctactc aggaggctgg ggcaggagaa tttcttgaac ccgggaggcg gaggttgcag
        943 3255
E--> 945 tgagccgaga tcacaccagt gcactccagc ctgggcaaca gagcaagacc cagtctcagg
        946 3315
E--> 948 aaaaaaaaaa aaaa
        949 3329
        952 <210> SEQ ID NO: 6
        953 <211> LENGTH: 2276
        954 <212> TYPE: DNA
        955 <213> ORGANISM: Homo sapiens
        957 <220> FEATURE:
        958 <221> NAME/KEY: CDS
        959 <222> LOCATION: (103)..(486)
        961 <400> SEQUENCE: 6
E--> 962 ctgaactggg agtcaggtgg ttgacttgtg cctggctgca gtagcagcgg catctccctt
        963 60
E--> 965 gcacagttct cctcctcggc ctgcccaaga gtccaccagg cc atg gac gca gtg
        966 114
```

```
     967                                        Met Asp Ala Val
     968                                         1
E--> 970 gct gtg tat cat ggc aaa atc agc agg gaa acc ggc gag aag ctc ctg
     971 162
     972 Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly Glu Lys Leu Leu
     973   5              10             15                    20
E--> 975 ctt gcc act ggg ctg gat ggc agc tat ttg ctg agg gac agc gag agc
     976 210
     977 Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg Asp Ser Glu Ser
     978              25             30             35
E--> 980 gtg cca ggc gtg tac tgc cta tgt gtg ctg tat cac ggt tac att tat
     981 258
     982 Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His Gly Tyr Ile Tyr
     983           40             45             50
E--> 985 aca tac cga gtg tcc cag aca gaa aca ggt tct tgg agt gct gag aca
     986 306
     987 Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp Ser Ala Glu Thr
     988           55             60             65
E--> 990 gca cct ggg gta cat aaa aga tat ttc cgg aaa ata aaa aat ctc att
     991 354
     992 Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile Lys Asn Leu Ile
     993        70             75             80
E--> 995 tca gca ttt cag aag cca gat caa ggc att gta ata cct ctg cag tat
     996 402
     997 Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile Pro Leu Gln Tyr
     998 85             90             95             100
E--> 1000 cca gtt gag aag aag tcc tca gct aga agt aca caa ggt act aca ggg
     1001 450
     1002 Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln Gly Thr Thr Gly
     1003              105            110            115
E--> 1005 ata aga gaa gat cct gat gtc tgc ctg aaa gcc cca tgaagaaaaa
     1006 496
     1007 Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro
     1008           120            125
E--> 1010 taaaacacct tgtactttat tttctataat ttaaatatat gctaagtctt atatattgta
     1011 556
E--> 1013 gataatacag ttcggtgagc tacaaatgca tttctaaagc cattgtagtc ctgtaatgga
     1014 616
E--> 1016 agcatctagc atgtcgtcaa agctgaaatg gactttgta catagtgagg agctttgaaa
     1017 676
E--> 1019 cgaggattgg gaaaagtaat tccgtaggtt attttcagtt attatattta caaatgggaa
     1020 736
E--> 1022 acaaaaggat aatgaatact ttataaagga ttaatgtcaa ttcttgccaa atataaataa
     1023 796
E--> 1025 aaataatcct cagtttttgt gaaaagctcc atttttagta aaatattatt ttatagctac
     1026 855
E--> 1028 taattttaaa atgtcttgct tgattgtatg gtgggaagtt ggctggtgtc ccttgtcttt
     1029 916
E--> 1031 gccaagttct ccactagcta tggtgtcata ggctcttttg ggatttttga agctgtatac
```

```
      1032 976
E--> 1034 tgtgtgctaa aacaagcact aaacaaagag tgaaggattt atgtttaatt ctgaaagcaa
      1035 1036
E--> 1037 ccttcttgcc tagtgttctg atattggaca gtaaaatcca cagaccaacc tggagttgaa
      1038 1096
E--> 1040 aatcttataa tttaaaatat gctctaaaca tgtttatcgt atttgatgct acaggatttg
      1041 1156
E--> 1043 aaattgtatt acaaatccaa tgaaatgagt ttttcttttc atttacctct gccccagttg
      1044 1216
E--> 1046 tttctactac atggaagacc tcattttgaa gggaaatttc agcagctgca gctcatgagt
      1047 1276
E--> 1049 aactgatttg taacaagcct ccttttaaag taaccctaca aaaccactgg aaagtttatg
      1050 1336
E--> 1052 gttgtattat ttttaaaaa aattccaagt gattgaaact tacacgagat acagaatttt
      1053 1396
E--> 1055 atgcggcatt ttcttctcac atttatattt ttgtgatttt gtgattgatt atatgtcact
      1056 1456
E--> 1058 ttgctacagg gctcacagaa ttcattcact caacaaacat aatagggcgc tgagggcata
      1059 1516
E--> 1061 gaagtaaaaa cacctggtcc ctgctctcag ttcactgtct tgttggacga gaaaacaata
      1062 1576
E--> 1064 acgataaaag acagtgaaag aaaataacga taaaagacag tgaaagaaaa taacaataaa
      1065 1636
E--> 1067 agacaaggaa aaaataacaa tgaaagttga taagtacatg ataagcgagg ttccccgtgt
      1068 1696
E--> 1070 gtaggtagat ctggtcttta gaggcagata gataggtcag tgcaaatact ctggtccatg
      1071 1756
E--> 1073 ggccatatga aaaggctaag cttcactgta aaataataac tgggaattct gggttgtgta
      1074 1816
E--> 1076 tgggtgttgg tgaacttggt tttaattagt gaactgctga gagacagagc tattctccat
      1077 1876
E--> 1079 gtactggcaa gacctgattt ctgagcattt aatatggatg ccgtgggagt acaaaagtgg
      1080 1936
E--> 1082 agtgtggcct gagtaatgca ttatgggtgg tttaccattt cttgaggtaa aagcatcaca
      1083 1996
E--> 1085 tgaacttgta aaggaattta aaaatcctac tttcataata agttgcatag gtttaataat
      1086 2056
E--> 1088 ttttaattat atggcttgag tttaaattgt aataggcgta actaatttta actctataat
      1089 2116
E--> 1091 gtgttcattc tggaataatc ctaaacatat gaattatgtt tgcatgttca cttccaagag
      1092 2176
E--> 1094 ccttttttg aaaaaaagct ttttttgaat catcaagtct ttcacattta aataaagtgt
      1095 2236
E--> 1097 ttgaaagctt tatttaaaaa aaaaaaaaaa aaaaaaaaaa
      1098 2276
      1101 <210> SEQ ID NO: 7
      1102 <211> LENGTH: 4343
      1103 <212> TYPE: DNA
      1104 <213> ORGANISM: Homo sapiens
```

```
    1106 <220> FEATURE:
    1107 <221> NAME/KEY: CDS
    1108 <222> LOCATION: (1)..(1029)
    1110 <400> SEQUENCE: 7
E--> 1111 atg gac gcc cca aaa gca gga tac gcc ttt gag tac ctt att gaa aca
    1112 48
    1113 Met Asp Ala Pro Lys Ala Gly Tyr Ala Phe Glu Tyr Leu Ile Glu Thr
    1114   1               5               10              15
E--> 1116 tta aat gac agt tca cat aag aag ttc ttc gat gta tct aaa ctt ggc
    1117 96
    1118 Leu Asn Asp Ser Ser His Lys Lys Phe Phe Asp Val Ser Lys Leu Gly
    1119           20              25              30
E--> 1121 acc aag tat gat gtt ctg cct tac tca ata cgg gtc ttg ttg gaa gct
    1122 144
    1123 Thr Lys Tyr Asp Val Leu Pro Tyr Ser Ile Arg Val Leu Leu Glu Ala
    1124           35              40              45
E--> 1126 gct gta cga aat tgt gat ggc ttt tta atg aag aag gaa gat gtt atg
    1127 192
    1128 Ala Val Arg Asn Cys Asp Gly Phe Leu Met Lys Lys Glu Asp Val Met
    1129           50              55              60
E--> 1131 aac att tta gac tgg aaa acc aaa caa agc aat gtt gaa gtg ccc ttt
    1132 240
    1133 Asn Ile Leu Asp Trp Lys Thr Lys Gln Ser Asn Val Glu Val Pro Phe
    1134   65              70              75              80
E--> 1136 ttc cct gcc cgt gtt ctt ctt caa gat ttt act gga ata cca gca atg
    1137 288
    1138 Phe Pro Ala Arg Val Leu Leu Gln Asp Phe Thr Gly Ile Pro Ala Met
    1139           85              90              95
E--> 1141 gtg gat ttt gct gct atg agg gag gca gtg aaa act ctt gga ggt gat
    1142 336
    1143 Val Asp Phe Ala Ala Met Arg Glu Ala Val Lys Thr Leu Gly Gly Asp
    1144           100             105             110
E--> 1146 cct gag aaa gtc cat cct gct tgt ccg aca gat ctt aca gtt gac cat
    1147 384
    1148 Pro Glu Lys Val His Pro Ala Cys Pro Thr Asp Leu Thr Val Asp His
    1149           115             120             125
E--> 1151 tct tta caa att gac ttc agt aaa tgt gca ata cag aat gca cca aat
    1152 432
    1153 Ser Leu Gln Ile Asp Phe Ser Lys Cys Ala Ile Gln Asn Ala Pro Asn
    1154           130             135             140
E--> 1156 cct gga ggt ggt gac ctg cag aaa gca gga aag ctc tct cca ctt aaa
    1157 480
    1158 Pro Gly Gly Gly Asp Leu Gln Lys Ala Gly Lys Leu Ser Pro Leu Lys
    1159 145             150             155             160
E--> 1161 gtg cag cct aag aag ctt ccc tgc aga ggc cag act acc tgc cga gga
    1162 528
    1163 Val Gln Pro Lys Lys Leu Pro Cys Arg Gly Gln Thr Thr Cys Arg Gly
    1164           165             170             175
E--> 1166 tct tgt gat tct gga gaa cta ggc cga aac tca gga aca ttt tct tcg
```

```
      1167 576
      1168 Ser Cys Asp Ser Gly Glu Leu Gly Arg Asn Ser Gly Thr Phe Ser Ser
      1169             180             185             190
E--> 1171 cag att gag aat aca ccc atc ctg tgt cct ttt cat ttg caa cca gtg
      1172 624
      1173 Gln Ile Glu Asn Thr Pro Ile Leu Cys Pro Phe His Leu Gln Pro Val
      1174             195             200             205
E--> 1176 cct gaa cct gaa aca gtg tta aaa aat caa gaa gta gaa ttc ggc aga
      1177 672
      1178 Pro Glu Pro Glu Thr Val Leu Lys Asn Gln Glu Val Glu Phe Gly Arg
      1179         210             215             220
E--> 1181 aat cga gag agg ctt cag ttt ttt aag tgg agt tca aga gtt tta aag
      1182 720
      1183 Asn Arg Glu Arg Leu Gln Phe Phe Lys Trp Ser Ser Arg Val Leu Lys
      1184 225             230             235             240
E--> 1186 aat gtg gca gtg atc cct cct gga act gga atg gct cat caa ata aac
      1187 768
      1188 Asn Val Ala Val Ile Pro Pro Gly Thr Gly Met Ala His Gln Ile Asn
      1189             245             250             255
E--> 1191 tta gaa tat ttg tca aga gtg gtt ttt gaa gaa aaa gac ctc ctc ttc
      1192 816
      1193 Leu Glu Tyr Leu Ser Arg Val Val Phe Glu Glu Lys Asp Leu Leu Phe
      1194             260             265             270
E--> 1196 cca gac agt gta gtc ggc aca gat tca cac ata acg atg gtg aat ggt
      1197 864
      1198 Pro Asp Ser Val Val Gly Thr Asp Ser His Ile Thr Met Val Asn Gly
      1199             275             280             285
E--> 1201 tta ggg att ctg ggg tgg ggg gtt gga ggc att gaa aca gaa gca gtt
      1202 912
      1203 Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Thr Glu Ala Val
      1204         290             295             300
E--> 1206 atg ctt ggt ctg cca gtt tct ctt act tta cca gag gtg gtt gga tgt
      1207 960
      1208 Met Leu Gly Leu Pro Val Ser Leu Thr Leu Pro Glu Val Val Gly Cys
      1209 305             310             315             320
E--> 1211 gag tta act ggg tca tca aac cct ttt gtt aca tcc ata gat gtt gtt
      1212 1008
      1213 Glu Leu Thr Gly Ser Ser Asn Pro Phe Val Thr Ser Ile Asp Val Val
      1214             325             330             335
E--> 1216 ctt ggt att aca aag gta agt taaagttgtg gtagctctat gacttactga
      1217 1059
      1218 Leu Gly Ile Thr Lys Val Ser
      1219             340
E--> 1221 acattatttt tataaaaatt gaagagctct atgagagcag ggatttgggt tcattactgc
      1222 1119
E--> 1224 atcctcaggt ctcttgacgt tagccacatc atcatagtta tcatagtaat aacaacaaac
      1225 1179
E--> 1227 agagcattta gtttgtacta ataaatacaa agaaatttgt tgtgttcact tatgttagct
      1228 1239
```

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
E--> 1230 catttagtcc ttataacaag cctgtgagat ggatactatt actattctca ttgtaactct
     1231 1299
E--> 1233 gagaaaacta aggtacagta gggtttagtg acttaccaaa gggtcgaagg cctgagtata
     1234 1359
E--> 1236 aggggtagag caaagattcc aggcagtcag attcttgagt catgtctaac cattatgcct
     1237 1419
E--> 1239 tattagtgcc ttgttgcctt aataaacact tgctggacta catatttttt ttctcttttt
     1240 1479
E--> 1242 taacttgaat taaaaaaaaa tgtttagcaa aagttgawtg tgtcgtcttt aattaaatta
     1243 1539
E--> 1245 tttgcccgtt agaaactgtt gctctactaa gtaatgcttt caaaaacatg gactgtagaa
     1246 1599
E--> 1248 atgtgatata tcatttttct gttgccgttt taacatttct ctggattatt atgtaaaaat
     1249 1659
E--> 1251 cttctctctg aatttttaaa atactggctt cagaacttca atacatacac tgagcttgtt
     1252 1719
E--> 1254 aagcatatta atacacaggc tcacggattt cctagtgaac aataatttgt aactcttctt
     1255 1779
E--> 1257 cctaaatgtc tggcctttgc taactttatt ttaatgatta aatcctattt tgttaaatga
     1258 1839
E--> 1260 atgtacctgg aaaatgttcc acatataatt ccaatttgag tcccaatctc agcatttttg
     1261 1899
E--> 1263 gttagattat tggtacgaag gctttctgga tactccagtg taaggaaatg ataatgcctc
     1264 1959
E--> 1266 cctctcagca tttggtattg atccttcttc cctaattaga aaagaatttg gcatcttaga
     1267 2019
E--> 1269 gaaattattg attcaacgta tgataccaaa agatcaagta gtaaattggg aattgcagga
     1270 2079
E--> 1272 ttattcctag aggaaaagga gtatcccatt atgtttttac agaaatcaat tctttacttt
     1273 2139
E--> 1275 agacatcctg aaaactaacg ctgctttta gccttctcta gctgtttttt cctgacaata
     1276 2199
E--> 1278 ttactgtgtg tttttttgaca ttttagttta atgttaaaaa attaatctat tatatatgtt
     1279 2259
E--> 1281 tacatttatt gaatatattg attacttctt ttttgagatc ctgttccatt tgtgatcctt
     1282 2319
E--> 1284 ataggaataa tcctgtattg ttttttttgat gagagcagca tttggtttgt aatatctaat
     1285 2379
E--> 1287 ctgtgtttct ttcatcctaa aaaataaaac cataggccgg gcgcggtggc tcacgcctgt
     1288 2439
E--> 1290 aatcccagca ctttgggagg ccgaggcggg tggatcatga ggtcaggaga tcgagaccat
     1291 2499
E--> 1293 cctggctaac aaggtgaaac cccgtctcta ctaaaaatac aaaaaattag ccgggcgcgg
     1294 2559
E--> 1296 tggcgggcgc ctgtagtccc agcttctcgg gaggctgagg caggagaatg gcgtgaaccc
     1297 2619
E--> 1299 gggaggcgga gcttgcagtg agccaagatt gcgccactgc agtccgcagt ccggcctggg
     1300 2679
E--> 1302 cgacagagcg agactctgty tcaaaaaaaa aaaaaaaaaa aaaaaaacca taaatgagga
```

```
        1303 2739
E--> 1305 aacgcatctt tacacttagg gtttgagttt ctgtatctat aaaaaagggt ttggattaag
        1306 2799
E--> 1308 tgatccctgg cacttataaa atgttagggc ttaatattat tcatagatcg aggatagttt
        1309 2859
E--> 1311 cattcttagt cgcctcctta gtcactcttc ctataccaat ctgagaccat tttacaattt
        1312 2919
E--> 1314 agaaaagaca aataactggt tgggttactt gatagtataa taaccaagaa aaataatttt
        1315 2979
E--> 1317 agaaggaatt aagtttgaaa ccacatgtta acaaattcta ccaaagtggg atttgcctgt
        1318 3039
E--> 1320 gattaaagat gctgtaaaca tttgggccag tagttataat ttgaaaaatg tttatagcca
        1321 3099
E--> 1323 atatataatt ttttatttaa atatacagtt tcatcagtct attagtattt cattaagtct
        1324 3159
E--> 1326 aagatgccat cagtggttag caaacaccac tgtttatgc actgctaaga aagaataaag
        1327 3219
E--> 1329 ggctgtgtgc agtggctcac acctgtggga cgccaaggca ggagcatcac ttgaggccag
        1330 3279
E--> 1332 aagttcaaga ccaacctggt caacattgta agaccctgtc tctacaaaaa aaaaaaagtt
        1333 3339
E--> 1335 aaaaattagc tgggtgcggt ggcacatgcc tgtagttcca gctactctgg aggctaaggt
        1336 3399
E--> 1338 gggaggattg ctagagccac ggtgttggaa gctgcaatga gctgtgacca caccactgcg
        1339 3459
E--> 1341 ctccagcgtg ggcaacagag tgagaccctg tttctaaaag aaagaaagaa aaaagggctg
        1342 3519
E--> 1344 ccacctaaac agacacacta ttgagttgag gtaccctgat ttcaaagaca tgaaaatgtt
        1345 3579
E--> 1347 aattatagcc accttgaagc tttcaggscc ctttctaccc tgaattaaca gtgacattgg
        1348 3639
E--> 1350 accagtcttc tctttacttc ttatcttaaa atacccccaa aaccagaatg agttgattca
        1351 3699
E--> 1353 taaggacaat gaaggatctc attccttcac catcactagt attggttaaa aattttatt
        1354 3759
E--> 1356 tatagttttc agacaatcgt tgctaatctt atctttgcaa ttttgtatgt gtttctgtgt
        1357 3819
E--> 1359 attccttata tagcacctca ggcaagtagg agtggctgga aagtttgttg agtttttgg
        1360 3879
E--> 1362 aagtggagtt tcacaattat ctatagttga tcgaactaca atagcaaaca tgtgtccgga
        1363 3939
E--> 1365 atatggtgct atcctcagct ttttccctgt tgacaatgtg acattaaaac atttagaaca
        1366 3999
E--> 1368 tacaggtaag aagataaaag atcactagaa taaacatgtt acatttccaa tgtgtttgat
        1369 4059
E--> 1371 aatattttat aaattactac cttatccatg ttatttacta ctcacaaaat tacattatgt
        1372 4119
E--> 1374 tgaaacaaca actttcaagc aaacatcaga tgtctttaaa gagtgttgtg tcctcaaacc
        1375 4179
```

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
E--> 1377 ctagttccct gtgacacatt gaaagcaatt taaaggaatt attcaaacca ttgatcctga
     1378 4239
E--> 1380 cttgactgtt tcccataatg atggatacct cccctctac ttaggggtca taggtgcaat
     1381 4299
E--> 1383 ttaatggagt cagcccttaa acatattcac agcagtcccc ttct
     1384 4343
     1387 <210> SEQ ID NO: 8
     1388 <211> LENGTH: 55
     1389 <212> TYPE: DNA
     1390 <213> ORGANISM: Homo sapiens
     1392 <400> SEQUENCE: 8
E--> 1393 cacttataaa atgttagggc ttaatattat tcatagatcg aggatagttt cattcttagt
     1394      60
E--> 1396 cgcctcctta gtcactcttc ctataccaat ctgagaccat tttacaattt agaaaagaca
     1397     120
E--> 1399 aataactggt tgggttactt gatagtataa taacc
     1400     155
     1403 <210> SEQ ID NO: 9
     1404 <211> LENGTH: 278
     1405 <212> TYPE: DNA
     1406 <213> ORGANISM: Homo sapiens
     1408 <400> SEQUENCE: 9
E--> 1409 gaaggagaat atgaagaggt tagaaaagt cggtctg ttggtgaaat gaaggatgaa
     1410      60
E--> 1412 ggggaagaga cattaaatta tcctgatact accattgact tgtctcacct tcaaccccaa
     1413     120
E--> 1415 aggtccatcc agaaattggc ttcaaaagag gaatcttcta attctagtga cagtaaatca
     1416     180
E--> 1418 cagagccgga gacatttgtc agccaaggaa agaagggaaa tgaaaaagaa aaaacttcca
     1419     240
E--> 1421 agtgactcag gagatttaga agcgttagag ggaaagga
     1422     278
     1425 <210> SEQ ID NO: 10
     1426 <211> LENGTH: 135
     1427 <212> TYPE: DNA
     1428 <213> ORGANISM: Homo sapiens
     1430 <400> SEQUENCE: 10
E--> 1431 ttctgacaat gagtaagaag aaagagggtc ttgccctttg gttattaaga tttatcatag
     1432      60
E--> 1434 agcaataata astaaatcgg tgttatacca gcacagagat tagacaaata aaccaaggga
     1435     120
E--> 1437 ctggactaaa taagc
     1438     135
     1441 <210> SEQ ID NO: 11
     1442 <211> LENGTH: 197
     1443 <212> TYPE: DNA
     1444 <213> ORGANISM: Homo sapiens
     1446 <400> SEQUENCE: 11
E--> 1447 atggtaccca gtttcaaatt aacatggtta ttttacttgt gttcccaaat ttaacattag
```

see item 10 on Exa Summary Sheet
name
format
error

```
         1448     60
E--> 1450 ggaatttttg gttgtgggtc tgttatcact agaaaaatat atatattggt gctgaagata
         1451    120
E--> 1453 attttgagat aattagacaa gacagtttag catttacaag aacaagtttg gcagttgaag
         1454    180
E--> 1456 aatctattta tatgact
         1457    197
         1460 <210> SEQ ID NO: 12
         1461 <211> LENGTH: 137
         1462 <212> TYPE: DNA
         1463 <213> ORGANISM: Homo sapiens
         1465 <400> SEQUENCE: 12
E--> 1466 ccaccgcacc tggctgatgc ttttctatct gacttctttc agaggaccct gaaagacact
         1467     60
E--> 1469 aagtggaatc tttccttgaa gtcttccaag ctaaaacaat tctctggaaa gatcacctct
         1470    120
E--> 1472 gttcagtcct ggtctct
         1473    137
         1476 <210> SEQ ID NO: 13
         1477 <211> LENGTH: 274
         1478 <212> TYPE: DNA
         1479 <213> ORGANISM: Homo sapiens
         1481 <400> SEQUENCE: 13
E--> 1482 cgtttacaga ttctcttgcg gctggcggtg gaactacaaa gggatcggtg cctatatcac
         1483     60
E--> 1485 aataccaaac ttgataataa tctagattct gtgtytctgc ttatagacca tgtttgtagt
         1486    120
E--> 1488 aggtaagagg aaaacttcct atattctgaa acagcctaac attttacaaa attttagttt
         1489    180
E--> 1491 tcttttttag agtcttatcc tgtagctata taacagttca tgtctgattt agcatttgtt
         1492    240
E--> 1494 cacgagtaaa gctggaacta tgaaaattga aaat
         1495    274
         1498 <210> SEQ ID NO: 14
         1499 <211> LENGTH: 171
         1500 <212> TYPE: DNA
         1501 <213> ORGANISM: Homo sapiens
         1503 <400> SEQUENCE: 14
E--> 1504 gattaggtga ccttccttga aragccacgg gtttcccata tcgaaatgct attcattacc
         1505     60
E--> 1507 cgagtcacct angttcttac aaaggaagcg agaaaattgc ttttgttggg ccatgccct
         1508    120
E--> 1510 tttgcanngg ttcctaagta tagtcgccan aattttttta atggcctaaa g
         1511    171
         1514 <210> SEQ ID NO: 15
         1515 <211> LENGTH: 161
         1516 <212> TYPE: DNA
         1517 <213> ORGANISM: Homo sapiens
         1519 <400> SEQUENCE: 15
```

see
Item 10 and item 1

RAW SEQUENCE LISTING   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:46

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
E--> 1520 aggggcgctt gttctgctct cagcagattg gttacacgcg tcaggtggtg gcgatgactt
     1521    60
E--> 1523 aattcctagc ccaagaagaa tataatgtta aaactggtta tgtaattttt gtgcctctcc
     1524   120
E--> 1526 tttttaatgc agtatttagt tcagatgttg gcgatttttc a
     1527   161
     1530 <210> SEQ ID NO: 16
     1531 <211> LENGTH: 323
     1532 <212> TYPE: DNA
     1533 <213> ORGANISM: Homo sapiens
     1535 <400> SEQUENCE: 16
E--> 1536 tataaggwgg gaaccttact atctctaatg accttactga tgctgacttt aatactctgt
     1537    60
E--> 1539 gaaggttaga gttcagtgaa tgttacctag aaacagcccc ggctgtggaa tactttattc
     1540   120
E--> 1542 ttagccctat atttgggtt tggatgtcca ctgtgctggt tcccagagat agtaagggga
     1543   180
E--> 1545 tgagagtatt ggttacatct cctgacccac atacttaaga tccagatgaa caagacagtt
     1546   240
E--> 1548 ttcactcctg cttggtagaa cctatttgyk shaggaaaca gytcctaaag aatggttcta
     1549   300
E--> 1551 gccagaccct gtcgytacca gaa
     1552   323
     1555 <210> SEQ ID NO: 17
     1556 <211> LENGTH: 138
     1557 <212> TYPE: DNA
     1558 <213> ORGANISM: Homo sapiens
     1560 <400> SEQUENCE: 17
E--> 1561 agtatgacaa atagtttctg cctgattggt gagatttggg atgggccccc actttgtttc
     1562    60
E--> 1564 tctttctgca taaaaatttc aacattttta caaaattttc aaaaacttct cctcagtctg
     1565   120
E--> 1567 tacatctttg ttaatcag
     1568   138
     1571 <210> SEQ ID NO: 18
     1572 <211> LENGTH: 135
     1573 <212> TYPE: DNA
     1574 <213> ORGANISM: Homo sapiens
     1576 <400> SEQUENCE: 18
E--> 1577 tgatccccac aatttcttgt gattggtgag gaactataaa tgactcccat ccaagcttat
     1578    60
E--> 1580 accagaaaaa aggagcacat tttctacaaa ttatatcatt tttaatccat taccacatta
     1581   120
E--> 1583 ttttaggg ga actac
     1584   135
     1587 <210> SEQ ID NO: 19
     1588 <211> LENGTH: 219
     1589 <212> TYPE: DNA
     1590 <213> ORGANISM: Homo sapiens
```

```
        1592 <400> SEQUENCE: 19
E--> 1593 ctgagaggag ccatgtatac aaaccacttt ttctaacatg gtctttatta aactttgaat
        1594    60
E--> 1596 ataagtacac ctgctcgaag tgttcatcta tattatttaa gaacaagcaa ctgtaaaaca
        1597    120
E--> 1599 gtaaaatcac aaaaggtaag ttgttggaag acaacaaaaa agaattacta tatctgatcc
        1600    180
E--> 1602 tgcgtgttta ttttagaatc tgttaatagg cctacagct
        1603    219
        1606 <210> SEQ ID NO: 20
        1607 <211> LENGTH: 191
        1608 <212> TYPE: DNA
        1609 <213> ORGANISM: Homo sapiens
        1611 <400> SEQUENCE: 20
E--> 1612 acagtgagtg tggctgaaac ctaagctgaa ggaagggagg agcaggcact gccatgaggg
        1613    60
E--> 1615 gtccctggac agaaactctt cagcaggcct tgaagtttag ttcaggggct acatggaata.
        1616    120
E--> 1618 ccactattta gcacacaggt gtgatctgag gtgagggact acctttcga tcttggtttt
        1619    180
E--> 1621 ctcatttatt t
        1622    191
        2221 <210> SEQ ID NO: 43
        2222 <211> LENGTH: 244
        2223 <212> TYPE: DNA
        2224 <213> ORGANISM: Homo sapiens
        2226 <400> SEQUENCE: 43
E--> 2227 tactcttcaa ccatgatttt tctctgatgg cctgtgtgaa cagattaatg gtgtccatct
        2228    60
E--> 2230 aattccttcc ccactggggg aaagcaaatc atcaggccca ttgcaaaaac tgctcttggt
        2231    120
E--> 2233 tgagcttcct gccttaaatc atacccacag tgaatggcgt ccctttatca ccgctaatga
        2234    180
E--> 2236 ctctgacatc tctctccact cacatgtgag cctcctcagc tctcganaaa caagtcngtc
        2237    240
E--> 2239 tcgg
        2240    244
```

FYI!

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

<pre>
VERIFICATION SUMMARY   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:48

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw
</pre>

<pre>
L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:58 SEQ:1
M:254 Repeated in SeqNo-1
L:295 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
M:254 Repeated in SeqNo-2
L:467 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:649 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4
M:254 Repeated in SeqNo=4
L:759 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
M:254 Repeated in SeqNo=5
L:962 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:6
M:254 Repeated in SeqNo=6
L:1111 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:7
M:254 Repeated in SeqNo=7
L:1393 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:8
M:254 Repeated in SeqNo=8
L:1409 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:1409 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:1409 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:1409 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:1409 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:1409 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:9
M:254 Repeated in SeqNo=9
L:1431 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:10
M:254 Repeated in SeqNo=10
L:1447 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:11
M:254 Repeated in SeqNo-11
L:1466 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:12
M:254 Repeated in SeqNo-12
L:1482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13
M:254 Repeated in SeqNo=13
L:1504 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:14
L:1507 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:1507 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:1507 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:1507 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
M:340 Repeated in SeqNo=14
M:254 Repeated in SeqNo=14
L:1510 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:1510 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:1510 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:1510 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:1520 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15
M:254 Repeated in SeqNo=15
L:1536 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:16
M:254 Repeated in SeqNo=16
</pre>

VERIFICATION SUMMARY   DATE: 12/21/2000
PATENT APPLICATION: US/09/730,559   TIME: 09:06:48

Input Set : A:\766.21 CIP sequence.txt
Output Set: N:\CRF3\12212000\I730559.raw

```
L:1561 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:17
M:254 Repeated in SeqNo-17
L:1577 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:18
M:254 Repeated in SeqNo=18
L:1593 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:1612 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:20
M:254 Repeated in SeqNo=20
L:1631 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:21
M:254 Repeated in SeqNo=21
L:1647 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:22
M:254 Repeated in SeqNo=22
L:1672 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:23
M:254 Repeated in SeqNo=23
L:1697 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:24
M:254 Repeated in SeqNo=24
L:1716 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:25
M:254 Repeated in SeqNo=25
L:1851 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:1851 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:1851 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:1851 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
L:1851 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:2180 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:41
L:2180 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:41
L:2180 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:41
L:2180 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:41
L:2180 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:41
L:2236 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:43
L:2236 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:2236 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
L:2236 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:43
M:340 Repeated in SeqNo=43
L:2249 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:44
L:2249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:44
L:2249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:44
L:2249 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:44
L:2249 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:44
L:3185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115
L:3200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116
L:3254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120
```